

SEQUENCE LISTING

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 Toma, Salvatore
 Isacchi, Antonella

<120> Tankyrase Homolog Protein (THP), Nucleic Acids, And Methods Related To The Same

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 <141> 2000-07-03

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<170> PatentIn version 3.1

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Tyr Thr	His Arg Arg Lys Glu Val Ser Glu Glu Asn	His Asn His	
1010	1015	1020	
gcc aat	gaa cga atg cta ttt cat ggg tct cct ttt	gtg aat gca	3114
Ala Asn	Glu Arg Met Leu Phe His Gly Ser Pro Phe	Val Asn Ala	
1025	1030	1035	
att atc	cac aaa ggc ttt gat gaa agg cat gcg tac	ata ggt ggt	3159
Ile Ile	His Lys Gly Phe Asp Glu Arg His Ala Tyr	Ile Gly Gly	
1040	1045	1050	
atg ttt	gga gct ggc att tat ttt gct gaa aac tct	tcc aaa agc	3204
Met Phe	Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser	Ser Lys Ser	
1055	1060	1065	
aat caa	tat gta tat gga att gga gga ggt act ggg	tgt cca gtt	3249
Asn Gln	Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly	Cys Pro Val	
1070	1075	1080	
cac aaa	gac aga tct tgt tac att tgc cac agg cag	ctg ctc ttt	3294
His Lys	Asp Arg Ser Cys Tyr Ile Cys His Arg Gln	Leu Leu Phe	
1085	1090	1095	
tgc cgg	gta acc ttg gga aag tct ttc ctg cag ttc	agt gca atg	3339
Cys Arg	Val Thr Leu Gly Lys Ser Phe Leu Gln Phe	Ser Ala Met	
1100	1105	1110	
aaa atg	gca cat tct cct cca ggt cat cac tca gtc	act ggt agg	3384
Lys Met	Ala His Ser Pro Pro Gly His His Ser Val	Thr Gly Arg	
1115	1120	1125	
ccc agt	gta aat ggc cta gca tta gct gaa tat gtt	att tac aga	3429
Pro Ser	Val Asn Gly Leu Ala Leu Ala Glu Tyr Val	Ile Tyr Arg	
1130	1135	1140	
gga gaa	cag gct tat cct gag tat tta att act tac	cag att atg	3474
Gly Glu	Gln Ala Tyr Pro Glu Tyr Leu Ile Thr Tyr	Gln Ile Met	
1145	1150	1155	
agg cct	gaa ggt atg gtc gat gga		3498
Arg Pro	Glu Gly Met Val Asp Gly		
1160	1165		

<210> 5
 <211> 1166
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 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (368)..(368)
 <223> The 'Xaa' at location 368 stands for Met, Val, or Leu.

<220>
 <221> misc_feature
 <222> (392)..(392)
 <223> The 'Xaa' at location 392 stands for Asn, or Thr.

<220>
 <221> misc_feature
 <222> (415)..(415)
 <223> The 'Xaa' at location 415 stands for Val, or Ile.

<220>
 <221> misc_feature
 <222> (558)..(558)
 <223> The 'Xaa' at location 558 stands for Gly, or Glu.

<220>

<221> misc feature
 <222> (559)..(559)
 <223> The 'Xaa' at location 559 stands for Gly, or Ala.

 <220>
 <221> misc feature
 <222> (764)..(764)
 <223> The 'Xaa' at location 764 stands for Val, or Leu.

 <220>
 <221> misc feature
 <222> (884)..(884)
 <223> The 'Xaa' at location 884 stands for Asn, Asp, His, or Tyr.

 <220>
 <223> PCR Primers

 <220>
 <221> misc feature
 <222> (1102)..(1102)
 <223> N is any nucleic acid

 <220>
 <221> misc feature
 <222> (2650)..(2650)
 <223> N is any nucleic acid

 <400> 5

Met Ser Gly Arg Arg Cys Ala Gly Gly Gly Ala Ala Cys Ala Ser Ala
 1 5 10 15

Ala Ala Glu Ala Val Glu Pro Ala Ala Arg Glu Leu Phe Glu Ala Cys
 20 25 30

Arg Asn Gly Asp Val Glu Arg Val Lys Arg Leu Val Thr Pro Glu Lys
 35 40 45

Val Asn Ser Arg Asp Thr Ala Gly Arg Lys Ser Thr Pro Leu His Leu
 50 55 60

Ala Ala Gly Phe Gly Arg Lys Asp Val Val Glu Tyr Leu Leu Gln Asn
 65 70 75 80

Gly Ala Asn Val Gln Ala Arg Asp Asp Gly Gly Leu Ile Pro Leu His
 85 90 95

Asn Ala Cys Ser Phe Gly His Ala Glu Val Val Asn Leu Leu Leu Arg
 100 105 110

His Gly Ala Asp Pro Asn Ala Arg Asp Asn Trp Asn Tyr Thr Pro Leu
 115 120 125

His Glu Ala Ala Ile Lys Gly Lys Ile Asp Val Cys Ile Val Leu Leu
 130 135 140

Gln His Gly Ala Glu Pro Thr Ile Arg Asn Thr Asp Gly Arg Thr Ala
 145 150 155 160

Leu Asp Leu Ala Asp Pro Ser Ala Lys Ala Val Leu Thr Gly Glu Tyr
 165 170 175

Lys Lys Asp Glu Leu Leu Glu Ser Ala Arg Ser Gly Asn Glu Glu Lys
180 185 190

Met Met Ala Leu Leu Thr Pro Leu Asn Val Asn Cys His Ala Ser Asp
195 200 205

Gly Arg Lys Ser Thr Pro Leu His Leu Ala Ala Gly Tyr Asn Arg Val
210 215 220

Lys Ile Val Gln Leu Leu Leu Gln His Gly Ala Asp Val His Ala Lys
225 230 235 240

Asp Lys Gly Asp Leu Val Pro Leu His Asn Ala Cys Ser Tyr Gly His
245 250 255

Tyr Glu Val Thr Glu Leu Leu Val Lys His Gly Ala Cys Val Asn Ala
260 265 270

Met Asp Leu Trp Gln Phe Thr Pro Leu His Glu Ala Ala Ser Lys Asn
275 280 285

Arg Val Glu Val Cys Ser Leu Leu Leu Ser Tyr Gly Ala Asp Pro Thr
290 295 300

Leu Leu Asn Cys His Asn Lys Ser Ala Ile Asp Leu Ala Pro Thr Pro
305 310 315 320

Gln Leu Lys Glu Arg Leu Ala Tyr Glu Phe Lys Gly His Ser Leu Leu
325 330 335

Gln Ala Ala Arg Glu Ala Asp Val Thr Arg Ile Lys Lys His Leu Ser
340 345 350

Leu Glu Met Val Asn Phe Lys His Pro Gln Thr His Glu Thr Ala Xaa
355 360 365

His Cys Ala Ala Ala Ser Pro Tyr Pro Lys Arg Lys Gln Ile Cys Glu
370 375 380

Leu Leu Leu Arg Lys Gly Ala Xaa Ile Asn Glu Lys Thr Lys Glu Phe
385 390 395 400

Leu Thr Pro Leu His Val Ala Ser Glu Lys Ala His Asn Asp Xaa Val
405 410 415

Glu Val Val Val Lys His Glu Ala Lys Val Asn Ala Leu Asp Asn Leu
420 425 430

Gly Gln Thr Ser Leu His Arg Ala Ala Tyr Cys Gly His Leu Gln Thr
435 440 445

Cys Arg Leu Leu Leu Ser Tyr Gly Cys Asp Pro Asn Ile Ile Ser Leu

450

455

460

Gln Gly Phe Thr Ala Leu Gln Met Gly Asn Glu Asn Val Gln Gln Leu
465 470 475 480

Leu Gln Glu Gly Ile Ser Leu Gly Asn Ser Glu Ala Asp Arg Gln Leu
485 490 495

Leu Glu Ala Ala Lys Ala Gly Asp Val Glu Thr Val Lys Lys Leu Cys
500 505 510

Thr Val Gln Ser Val Asn Cys Arg Asp Ile Glu Gly Arg Gln Ser Thr
515 520 525

Pro Leu His Phe Ala Ala Gly Tyr Asn Arg Val Ser Val Val Glu Tyr
530 535 540

Leu Leu Gln His Gly Ala Asp Val His Ala Lys Asp Lys Xaa Xaa Leu
545 550 555 560

Val Pro Leu His Asn Ala Cys Ser Tyr Gly His Tyr Glu Val Ala Glu
565 570 575

Leu Leu Val Lys His Gly Ala Val Val Asn Val Ala Asp Leu Trp Lys
580 585 590

Phe Thr Pro Leu His Glu Ala Ala Ala Lys Gly Lys Tyr Glu Ile Cys
595 600 605

Lys Leu Leu Leu Gln His Gly Ala Asp Pro Thr Lys Lys Asn Arg Asp
610 615 620

Gly Asn Thr Pro Leu Asp Leu Val Lys Asp Gly Asp Thr Asp Ile Gln
625 630 635 640

Asp Leu Leu Arg Gly Asp Ala Ala Leu Leu Asp Ala Ala Lys Lys Ser
645 650 655

Cys Leu Ala Arg Val Lys Lys Leu Ser Ser Pro Asp Asn Val Asn Cys
660 665 670

Arg Asp Thr Gln Gly Arg His Ser Thr Pro Leu His Leu Ala Ala Gly
675 680 685

Tyr Asn Asn Leu Glu Val Ala Glu Tyr Leu Leu Gln His Gly Ala Asp
690 695 700

Val Asn Ala Gln Asp Lys Gly Gly Leu Ile Pro Leu His Asn Ala Ala
705 710 715 720

Ser Tyr Gly His Val Asp Val Ala Ala Leu Leu Ile Lys Tyr Asn Ala
725 730 735

Cys Val Asn Ala Thr Asp Lys Trp Ala Phe Thr Pro Leu His Glu Ala
 740 745 750
 Ala Gln Lys Gly Arg Thr Gln Leu Cys Ala Leu Xaa Leu Ala His Gly
 755 760 765
 Ala Asp Pro Thr Leu Lys Asn Gln Glu Gly Gln Thr Pro Leu Asp Leu
 770 775 780
 Val Ser Ala Asp Asp Val Ser Ala Leu Leu Thr Ala Ala Met Pro Pro
 785 790 795 800
 Ser Ala Leu Pro Ser Cys Tyr Lys Pro Gln Val Leu Asn Gly Val Arg
 805 810 815
 Ser Pro Gly Ala Thr Ala Asp Ala Leu Ser Ser Gly Pro Ser Ser Pro
 820 825 830
 Ser Ser Leu Ser Ala Ala Ser Ser Leu Asp Asn Leu Ser Gly Ser Phe
 835 840 845
 Ser Glu Leu Ser Ser Val Val Ser Ser Ser Gly Thr Glu Gly Ala Ser
 850 855 860
 Ser Leu Glu Lys Lys Glu Val Pro Gly Val Asp Phe Ser Ile Thr Gln
 865 870 875 880
 Phe Val Arg Xaa Leu Gly Leu Glu His Leu Met Asp Ile Phe Glu Arg
 885 890 895
 Glu Gln Ile Thr Leu Asp Val Leu Val Glu Met Gly His Lys Glu Leu
 900 905 910
 Lys Glu Ile Gly Ile Asn Ala Tyr Gly His Arg His Lys Leu Ile Lys
 915 920 925
 Gly Val Glu Arg Leu Ile Ser Gly Gln Gln Gly Leu Asn Pro Tyr Leu
 930 935 940
 Thr Leu Asn Thr Ser Gly Ser Gly Thr Ile Leu Ile Asp Leu Ser Pro
 945 950 955 960
 Asp Asp Lys Glu Phe Gln Ser Val Glu Glu Glu Met Gln Ser Thr Val
 965 970 975
 Arg Glu His Arg Asp Gly Gly His Ala Gly Gly Ile Phe Asn Arg Tyr
 980 985 990
 Asn Ile Leu Lys Ile Gln Lys Val Cys Asn Lys Lys Leu Trp Glu Arg
 995 1000 1005
 Tyr Thr His Arg Arg Lys Glu Val Ser Glu Glu Asn His Asn His
 1010 1015 1020

Ala Asn Glu Arg Met Leu Phe His Gly Ser Pro Phe Val Asn Ala
1025 1030 1035

Ile Ile His Lys Gly Phe Asp Glu Arg His Ala Tyr Ile Gly Gly
1040 1045 1050

Met Phe Gly Ala Gly Ile Tyr Phe Ala Glu Asn Ser Ser Lys Ser
1055 1060 1065

Asn Gln Tyr Val Tyr Gly Ile Gly Gly Gly Thr Gly Cys Pro Val
1070 1075 1080

His Lys Asp Arg Ser Cys Tyr Ile Cys His Arg Gln Leu Leu Phe
1085 1090 1095

Cys Arg Val Thr Leu Gly Lys Ser Phe Leu Gln Phe Ser Ala Met
1100 1105 1110

Lys Met Ala His Ser Pro Pro Gly His His Ser Val Thr Gly Arg
1115 1120 1125

Pro Ser Val Asn Gly Leu Ala Leu Ala Glu Tyr Val Ile Tyr Arg
1130 1135 1140

Gly Glu Gln Ala Tyr Pro Glu Tyr Leu Ile Thr Tyr Gln Ile Met
1145 1150 1155

Arg Pro Glu Gly Met Val Asp Gly
1160 1165

<210> 6
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primers

<400> 6
cccgagagct gttcgaggc

19

<210> 7
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primers

<400> 7
caatctttac tctgttatat cct

23

<210> 8
<211> 41
<212> DNA
<213> Artificial Sequence
<220>

<223> PCR Primers

<400> 8

aagcggccgc attatggaaa ggatcatgtc gggtcgccgc t

41

<210> 9

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> PCR Primers

<400> 9

aaggatccac cataccttca ggcct

25

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> PCR Primers

<400> 10

aaaagcttta tggaaaggat catgtcgggt cgccgctgc

39